```
325  ysGlyGlyValAlaIleAlaIleGluAspSerGlyGluLeuSerLeuSerAla 341
     |||||||||||||||||||||||||||||||||||||||||
1056 AAGGAGGGGCAATTGCAATTCTAGATTCTGGAGAGATTAGCATTCTGCA 1105

342  AspSerGlyAspAlaValPheLeuGlyAsnThrValThrSerThrThr..  357
     |||:|||||||||:::|||||||||:||||||||||||
1105 GATCTCGGCGAATATCATTTTCGAGGGCAATACT...ACCAGCACTACAGG 1152

358  .......ProGlyThrAsnArgSerSerIleAspLeuGlyThrSerAlaL 372
     |||||||||||||||||||||||:||||||||
1153 AAGTCCTCGGAGTCGTGACCAGAAATGCTATAGATCTTCCATCGAATGCAA 1202

372  ysMetThrAlaLeuArgSerAlaAlaGlyArgAlaAlaIleThrTyrPheTyrAsp 388
     |||:||||||||||||||||||||||||||||||:|||
1203 AATTTTAAAATCTCCGAGCGACTCGGGAAATAAAGTTATTTCTATGAT 1252

389  ProIleThrThrGlySerSerThrThrValThrAspValLeuLysValAs 405
     ||||||||:::|||||||||||||||||||:|||:|||
1253 CCTATCACG........AGCTCAGGAGCTACTGAATAAGCTCTCTTGAA 1293

405  nGluThrProAlaAspSerAlaLeuGlnThrTyrThrGlyAsnIleIlePhe 422
     |:|||:||||||||||||||||||||||||:|||:||||:
1294 TAAAGCTGACGGCAGGATCTGGAAATACCTATGAAGGCTACATCGTTTTCT 1343

422  hrGlyGlyLeuLysSerGluThrGluAlaAlaAspSerLysAsnLeuThr 438
     |::||||||||||||||||||||||||||||||
1344 CTGGAGAGAAACTCTCAGAAGAGGAACTTAAGAAACCTGACAAATCTGAAG 1393

439  SerLysLeuLeuGlnProValThrLeuSerGlyGlyThrLeuSerLeuY 455
     |:::|||||||||||||||||:::|||||||||||
1394 TCTACAATTTACACAGGCTGTAGAGCTTGCCCAGTTGCCTTAGTTATTGAA 1443

455  sHisGlyValThrLeuGlnThrGlnAlaPheThrGlnGlnAlaAspSerA 472
     |||||||:|:|||||||||||||||||||||||:
1444 AGATGGAGTGACTGTAGTTGCAAATACTATAACGCAGTCGAGGGATCGA 1493

472  rgLeuGluMetAspValGlyThrThrLeuGlu...ProAlaAspThrSer 487
     ::::      |||||     |||:::
1494 AAGTCGTTATGGATGGGAGGGACTACTTTTGAGGCAAGCGCTGAGGGGGTC 1543

488  ThrIleAsnAsnLeuValIleLeuAsnIleSerSerIleAspGlyValAlaLysLy 504
     |||:||:::||||||||||||||||||||:||||
1544 ACTCTCAATGGCCTTAGCCATTAATATAGAATTCCTTAGATGGGACAAATAA 1593

504  sAlaLysIleGluThrLysLysAsnLeuThrLeuSerGlyT 521
     |||||||||||||||||||:||||
1594 AGCTATCAATAAAGGCGACCGGCAAGTAAGGAGTTCCCTTATCAGGGC 1643

521  hrIleThrLeuLeuAspProThrGlyThrPheTyrGluAsnHisSerLeu 537
     |||:||||||||||||||||||||||:||||
1644 CTATCATGCTTGTGAGATCCTCAGGGGACTAATATGACCATAAATCTC 1693

538  ArgAsnProGlnSerTyrAspIleLeuGluLeuLysAlaSerGlyThrVa 554
     |||   ||:::||||||||||||||||||||
1694 AGTCAACAGCAGGTCTTCCTTAATAGAGCTTTCTGCACAAGGAACGAT 1743

554  lThrSerThrAlaValThrProAspProIleMetGlyLeuLysPheHisT 571
     ||||    |||||||||||||||||||||||
1744 GACTACTACAGATACCCCGAATACCCAATTCTAAATACTACGAATCACT 1793

571  yrGlyTyrGlnGlyThrTrpGlyProGlyValTrp.......GlyThr 584
     |||:||||||||||||||||||:::|||
1794 ATGGGTTATCAAGGGAACTGGAAT...ATGTTTGGGTCGACGATGCAACT 1840

585  GlyAlaSerThrThrAlaThrPheAsnTrpThrHisThrGlyTyrIlePr 601
     |||||||||||||||:||||||||||||||||:|||
1841 GCAAAACAAAAAATCTACCTAACTGGACTAAAACAGGATACAAAGCC 1890

601  oAsnProGluArgIleGlySerLeuValProAsnSerLeuTrpAsnAlaP 618
     ||||||||||||||||||||||||||||:|||
1891 GAATCCAGAACGTCAGGAGCACAGACTTTGGTTCCTAATAGCCTGTGGGGTTCTT 1940
```

```
618  heIleAspIleSerSerLeuHisTyrLeuMetGluThrAlaAsnGluGly 634
     |:::|||||||||:::||||||||:::::|||:
1941 TTGTCGAATGTCCGGCTCCTCCATTCAGAGCGTCATACGGACCGGACGTTCG 1990

635  LeuGlnLeuGlyAspArgAlaPheThrProCysAlaGlyLeuSerAsnPhePheHi 651
     |||||||||||||:||||||||||||||||||:
1991 TTATCTTCGTCAACAAATTTGTGGGTATCAGGAAATCGCGGAGACTTTTTGCA 2040

651  sLysAspSerThrLysThrArgArgGlyGlyPheArgArgHisLeuSerGlyGlyT 668
     |||:::|||||||:|||||||||||:||||:|||:||||
2041 TGAAGATCAGAAAGGAAAACCAACGTAGTTATCGTCATTCTAGGCGCCGGGGTT 2090

668  yrValIleGlyGlyAsnLeuHisHisThrCysSerSerAspLysIleLeuSerAla 684
     |:::|||||||||||||||||:||||||||||::::||||:::|
2091 ATCCATTAGGAGCGGAGGATTCTCACGCGTTCTGAAAATTTCTTTAATTTT 2140

685  AlaPheCysGlnLeuPheGlyArgAspArgAspTyrPheValAlaLysAsp 701
     |:::|||||||||||||||||||:::|||||||||||:
2141 GCTTTTTGTCAGGTTTTTGGGCTACGACAAAGGACCATCTTGTGGCTAAGA 2190

701  nGlnGlyThrValTyrGlyValGlyThrLeuThrTyrTyrGlnHis....... 715
     ||||:||||||||||||||||||||||||:||:
2191 CCATACCCAATGTATATGCAGGGGCAATGAGTTACCGACACCTCGGAGAGT 2240

715  snGluThrTyrIleSerLeuProCysLysLeuArgProCysSerLeuSer 731
     |||:::|||:|||||||||||||||||||:
2241 CTAAGACCCTCGCTAAGAT............TIGTCA 2255

732  TyrValProThrGlyIleProValLeuPheSerGlyAsnLeuSerIleTyrTh 748
     :::||||||||||||||||||||||:::|
2257 GGAAATCTGAACTCCCTCACCTTTGTCTTCAATCGTGGTTTGCTTTATCG 2316

748  rHisThrAspSerAsnAspLeuHisLysTyrThrThrThrTyrProThrValL 765
     ||||||||||||||:::||||||||||||:|||
2317 CCATACCGACAATAACATGACCACAAGTACACTGGCTATTCTCCTGTTA 2356

765  ysGlySerTrpGlyAsnAspSerPheAlaLeuGluGlyGlyArgAla 781
     |||||||||||||||||||||||||||||:
2367 AGGGAAGCTGGGGAAATGATGCCTTCGGTATAGAATGTGGAGGAGCTAIC 2416

782  ProIleCysLeuAsp....GluSerAlaLeuPheGluGlnTyrMetProH 797
     :::|||||    |||||||||||:|||||
2417 CCGGTACATTGCTTCAGGACGTCGGGTCTTGGGTGGATACCACACCCATT 2456

797  eMetLysSerLeuGlnPheValTyrAlaHisGlnGluGlyPheLysGluGlnG 814
     |:::|||||||||||||||||||||||||||||||
2467 TCTAAACCTAGAGATGATCTATGCACATCAGAATGACTTTAAGGAAAACG 2515

814  lyThrGluAlaArgGluPheGlySerSerArgLeuValAsnLeuAlaLeu 830
     |||||||||||||||:||||||||||||:||:
2517 GCACAGAAGGCGCGTTCTTTCCAAAGTGAAGACCTCTTCAAATCTAGCGGT 2556

831  ProIleGlyIleArgPheAspLysGluSerAspCysSerGlnAspAlaThrTy 847
     |||||||||||||||||:::||||||||||||||:
2567 CCTGTAGGGATAAAAATTTGAGAAAATTCCGAT......AAGTCTACGTA 2610

847  rAsnLeuThrLeuGlyTyrThrValAspLeuValAlaArgSerAsnProAspc 854
     |:::||||||||||||||||||||||||:||
2611 TGATCTCTCCATAGCTTACGTTCCCGATGTGCTAAGTGTGTAATCAGGCT 2560

864  ysThrThrThrLeuArgIleSerGlyAspSerTrpLysThrPheGlyThr 880
     ||||||||||||||:|||||||||||||:||||
2651 GCACGACAAACTCTTATGGTTTCTGGGGATTCCTGGTCGACATGTGGTACA 2710

881  AsnLeuAlaArgGlnAlaLeuValLeuArgAlaGlyLysAsnHisPheCysPh 897
     |||||||||:::|||||||||||:||||||||:|||:
2711 AGTTTGCTGCTCAGACAAGCCTCTTCGTACGTGCTGGAAATCATCATGCCTT 2750

897  eAsnSerAsnPheGluAlaPheSerGlnPheSerPheGluLeuArgGlyS 914
     |||||||||||||||||||||||||||||
2751 TGCTCAAACTTTGAAGTTTTCAGTCACTTTGAAGTCAGTTGCGAGGTT 2810

914  erSerArgAsnTyrAsnValAspLeuGlyAlaLysTyrGlnPhe 928
     :::|||||||||/||| :::::||||||||||  |||
2811 CTTCTCGTAGCTATGCTATCGATCTTGGAGGAAGAATTCGGATTT 2854
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alignment_block:
US-09-428-122-2 × US-09-376-770-15

Align seg 1/1 to: US-09-376-770-15 from: 1 to: 2957

alignment_scores:
Quality: 2006.00   Length: 948
Ratio: 2.810   Gaps: 20
Percent Similarity: 75.316   Percent Identity: 45.570

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  1 MetLysSerPhenProLysPheValPheSerThrPheAlaIlePhePr   17
    |||::||||||::|::|||
101 ATGAGAATCGTCTTTTTCCTTGTTATTAATATCTTCATCCTAGCCTTTCC  150

 17 oLeuSerMetIle.............AlaThrGluThrValLeuAspSerS   30
    |||           |||                 |||::::|||  :::|||  |||
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151 TCTCTTAATGAGTGTTCTCCAGATGCTGCGGATCTCACATAGGGAGTC   200
 30 erAlaSerPheAspGlyAsn...LysAsnGlyAsnPheSerValArgGlu  45
    |||::::||||||    ||||||     :::::::::  |||||||
201 GTGACAGTTATAAATGGTGATACAAGCACCACAGAATTACTCCTAAAGCG  250

 46 SerGlnGluAspAla...GlyThrThrTyrLeuPheLysG::AsnValTh  5:
    :::  |||||::||||||       |||||||||:::  :::||||:|||:::
251 GCAACTTCTGAATGCTAGTGCCGACGACCTATATCTCGAGATGGGATGTCTC  30C

 61 rLeuGluAsnIleProGlyThrGlyThrAlaIleThrLysSerCysPheA  79
    :::|||||::::|||      |||  |||||||||||||||::::::::
301 GATAACCCAA...GCAGGGAAACAAACGAGCTTAACCACAAGTTGTTTTT  347

 78 snAsnThrLysGlyAspValAspPheGlyAsnGlyAsnSerLeuLeu  94
    ::|||||||  ||::::||||||||||    |||||||
348 CTAACACTGCAGGAAATCTTACCTTCTTAGGACACGGATTTTCTCTTCAT  397

 95 PheGlnThrValAspAlaGlyThrValAlaGlyIleAlaAlaValAsnSerSe  111
    |||      ::::::||||||||||||    |||||||
398 TTTGACAATATATTCGTCTACTGTTGCAGGTGTTGTTGCTAGCAAATAC  447

111 rValAlaAspLysSerThrThrPheIleGlyPheSerSerLeuSerPheI  128
    |||||||  ||||||||||      |||  |||||||
448 AGCAGCTTCTGGGATACGAAATTCTCAGGATTTCAACTCTTCGGATGC  497

128 leAlaSerProGlySerSerIleThrThrGlyLysGlyAlaValSerCys  144
    |||||||||||      |||||||||||:::  :::||:::
498 TTGCAGCTCCTAGG........ACCACAGGTAAAGGAGCCATTAAAATT  538

145 SerThrGlySerLeuSerLeuThrLysAsnValSerLeuLeuPheSerLy  161
    |||||||  |||  ||||||      ||||||
539 ACCGGATGGT...CTGGTGTTGAGACTATAGGAATTCGATCTTAATGA  585

161 sAsnPheSerThrAspAsnGlyValGlyAlaIleThrAlaLysThrLeuSer  178
    |::  ||||||||||||||||||:::  :::||||||||
586 AAATGCCTCTACTGAAAATGGGGAGCCATCAACACGAAGACTTTGTCTT  635

178 euThrGlyThrThrMetSerAlaLeuPheSerGluAsnThrSerSerLys  194
    |||||||      :::      ||||||||||||
636 TGACTGGGAGTACGCGGTTTGTTAGCTGCAATAGCTCGTCGCAA  685

195 LysGlyGlyAlaIleGlnThrSerAspAlaLeuThrIleThrGlyAsnGl  211
    |||||||||||||::  |||         |||||||||||
686 CAAGGGGGGAGCCAATCTATGCTTCGGTGACTCTGATTCTGAGAATGC  735

211 nGlyGluValSerPheSerArgAspAsnThrSerSerAspSerGlyAlaAlaI  228
    ::|||||||||||||||      |||   :::||||||
736 AGGAAATCTTGAGCTTCGGAACAACAGTGCGACAACATCAGGAGGCGGA  785

228 lePheThrGluAlaSerValThrIleSerAsnAsnAlaLysSerPhe  244
    |||  |::::||||||||      |||:::||||||
786 TCTCTGCTGAACGGAACCTTGTGATCTCCAATAACAAAATATCTTTTTC  835

245 IleAspAsnLysValThrGlyAlaSerSerThrThrGlyAspMetSe  261
    |||:::|||      |||      ::||||||
836 GATGGCTGCAAAGCAACT...ACAAA  858

261 rGlyGlyAlaIleLeuCysAlaThrTyrLys.....ThrSerThrAspThrLysSv  276
    ::||||||||||||||||::||:::|||      |||
859 TGGCGGAACCTATTGATTTCAACAAAGCAGGGCGGCAACCCAGACCCTATCT  908

276 alThrLeuThrGlyAsnGlnMetLeuLeuPheSerAsnAsnThrSerThr  292
    :::|||||||||||:::      |||::  |||||||
909 TGACTCTTTCAGGAAAATGAGAGCCCTGCATTTTCTGAATAACACAGCAGGA  959

293 ThrAlaGlyGlyAlaIleTyrValLysLysLeuGluLeuAlaSerGly..  308
    |||||||||||||||      ::|||||||
959 AATAGTGGAGGTCGGATTTATACCAAAAAATTGGTGTTGTATCCAGGACG  1008

309 .GlyLeuThrLeuPheSerArgAsnSerValAsnGlyGlyThrAlaProL  325
    |||  ::|||||||||||||||      |||||||||
1009 AGGAGGAGTGTTATTTCTAACAACAAAAGCTCGGAATGCTACT...CCTA  1055
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RESULT 12
P71133

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ID   P71133      PRELIMINARY;   PRT;   846 AA.
AC   P71133;
DT   01-FEB-1997 (TrEMBLrel. 02, Created)
DT   01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   POMP91B PRECURSOR.
OS   Chlamydophila psittaci.
OC   Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=OVINE ENZOOTIC ABORTION ISOLATE S26/3;
RX   MEDLINE; 96406378.
RA   Longbottom D., Russell M., Jones G.E., Lainson F.A., Herring A.J.;
RT   "Identification of a multigene family coding for the 90 kDa proteins
RT   of the ovine abortion subtype of Chlamydia psittaci.";
RL   FEMS Microbiol. Lett. 142:277-281(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=OVINE ENZOOTIC ABORTION ISOLATE S26/3;
RX   MEDLINE; 98187897.
RA   Longbottom D., Russell M., Dunbar S.M., Jones G.E., Herring A.J.;
RT   "Molecular cloning and characterization of the genes coding for the
RT   highly immunogenic cluster of 90-kilodalton envelope proteins from the
RT   Chlamydia psittaci subtype that causes abortion in sheep.";
RL   Infect. Immun. 66:1317-1324(1998).
DR   EMBL; U65943; AAC15923.1; -.
KW   Signal.
FT   SIGNAL         1     16       POTENTIAL.
FT   CHAIN         17    846       POMP91B.
SQ   SEQUENCE   846 AA;   90834 MW;   4CDC31DC03C2964E CRC64;
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Query Match   33.6%;   Score 1604.5;   DB 2;   Length 846;
Best Local Similarity 38.7%;   Pred. No. 1.8e-82;
Matches 368; Conservative 140;   Pred. No. 1.8e-82; Mismatches 269; Indels 173; Gaps 26;

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Qy   23  TETVLDSSASFPGN-KNGNFSVRESQEDAGTTYLFKGNVTLENIPGTGTAITKSCFNNTK  81
         ||| ||  :|     :|  ||  |:||       :||   :|: |  ||  |||::  :|
Db   26  TNETLTSSDSYNGNVTSDEFEVKET--TSGAIYTCEGNVCI-SYAGKDSPLNKSCFSETT  82

Qy   82  GDLTFTGNGNSLLFQTVDAGTVAGAAVNSSVVDKSTTFIGFS--SLSFIASPGSSTTTGK  139
         :| :| ||| :| | ::| |    ||  :   || : | |    ||| || |  ||  |
Db   83  ENLSFIGNGYTLCFDNTTQSSHPGAISVSGTNKILDISGFSLFSCAYCCPPG--TTGY  139

Qy   140 GAVSCSTGSLSLTKNVSLLFSKNFSTDNGAITAKTLSLTGTTMSALFSENTSSKKGGAI  199
         || |  ||: ||      |
Db   140 GAIQ-TKGTTLKDNSSLVFHKNCSTAEGGAIQCK--------------------------  173

Qy   200 QTSDALITIGNOGEVSFSDNTSSDSGAAIFTEASVTISNNAKVSFIDNKVTGASSSTTGD  259
                                                            :| |||
Db   174 --------------------------------------------------SSSSTAE  180

Qy   260 MSGGAICAYKTSTDTKVTLTGNQMLLFSNNTSTTRAGGAIYVKKLELASGGLTLFSRNSVN  319
         ||||||  |  | |  || ||||  |:::::  :||| ||||  |  | |||| || |  |:
Db   181 LK---------------LENNKNLVFSENSSKEKGGAIYADKLTIVSGGPTLFSNNSVS  224

Qy   320 GGTAPKGGAIAIEDS-GELSLSADSGDIVFLGNTVTST---TPGTNRSSIDLGTSAKMTA  375
         : :|||||| | :||  | || : | || |  | ::|    | ||| |||||| | | ||
Db   225 HNSSPKGGAICIKDSDGECSLTANLGDIFPDGNKIIITNGGSPIVTRNSIDLGSGGKFTK  284

Qy   376 LRSAAGRAIYFYDPI-TTGSSTTVTDVLKVNETPADSALQYTGNTVTST---TPGTN...  434
         | :| | ||:|||| |  ||||  | ||    :|  | | :|| ||  |    | |
Db   285 LNAKEGFGIFFYDPIANTGGSTEI---ELNKTESDTT--YTGKIVFSGEKLSDEEKTVP  338

Qy   435 KNLTSKLLQPVTLSGGTLSLKHGVTLLQTQAFTQQADSRLEMDVGTTLE----PADTSTIN  490
         :||:| :|||: | | || |  |||| : : : || |  :: | ||||      ||||| |
Db   339 ANLKSYFKQPLKIGAGSLVLKDGVTLEARKIITQTKGSTVVMDLGTTLLQTPSSSGETTLT  398

Qy   491 NLVINISSI---DGAKKAKIETKATSKNLTLSGTTLLDPTGTGFYENHSLRNPQSYDILE  547
         || :||:::   :|   | :  | :   |::::   :  | | :|| |  | : | :| |
Db   399 NLDINIASLGGGGGTAPAKLATNTPASQAISIA-AVNLVNTDSNTYEDPILSRASKSFSAI-  456

Qy   548 LKASGTVTSTAVTPDPIMGEKF----HYGVQGTWGPIVWGTGAST---TAFENWTKTGYI  600
             :||:|||| | | :  :    |||:||  | :| |:|||    ||| ||  ||:|
Db   457 ---TATTSSSTVTPPETNLKNYTPPTHYGYQGNW-TVTWKQGSSAQEKTATLTWEQTGYS  512

Qy   601 PNPERIGSLVPNSLWNNAFIDISSLHYLMETANEGLQOGDRAFWCAGLSNFFHKDSTKTRRG  660
         ||||:|||||||:||  || |  ::  :|  | || | |||| ::||:|||::| | | :|
Db   513 PNPERVGSLVPNTLWGAFSDTRAIQNLMDISVNGADYSRGFWVSSLANFLNKSGSDTKRK  572

Qy   661 FRHLSGGYVIGGNLHTCSDKILSAAFCQLFGRDRDYFVAKNQGTVYGGTLYQHNETYIS  720
         |||:||  |   |    |  | |||||||||:|:||||:||  |:| |::|||
Db   573 FRHSAGYALGVTAQTPSDDVCSAAFCQLFGKDKDYFVSKNSSTIYAGSIYQH------  626

Qy   721 LPCKLRPCSLSVPT---------EIPVLFSGGNLSYTHTDNDLKTKYT---------TY  761
                                 : | ::  || :| |  ::::|| |        |
Db   627 ------ISYWNTWNTLLQNTLGAEAPLVLNAQLTYCHASNNMKTNMTNTYTPKNVTP  677

Qy   762 PTVKGSWGNDSFALEFGGRAPICLDESALFEQYMPFKNKLQTFVYAHQEGFKEQGT-EAREF  820
         |::||:|||| | :||| :||| : ||:||:  |||  || : | |||: |||    :| |
Db   678 SEIKGDWGNDCFGVEFGAKAPI-ETASLLFDMYSPFVKLQLVHAHQDDFKENNSDQGRYF  736

Qy   821 GSSRLVNLALPTGIRFDKESDCQDDATYNLHLGYTVDLVRSNPDCTTTLRISGDS--WKTF  878
         |:| : ||::| :|:::   :   ||:||: | | :|:||||||| ::| :| :   | |
Db   737 ESNNLTNLSMPIGVKLEKFSHKDTASYNLTLAYAPDIVRSNPDCTASLLVSPTSAVWVIK  796

Qy   879 GTNLARQALVLRAGNHFCFNSNFEAFSQFSFELRGSSRNNNVDLGAKYQF  928
         |:|||: | :|:|||  | |:|:||||| |||||| | ::|:|||:| ||
Db   797 ANNLARHAFILQAGNVLALTRNTELFSQFGFELRGSCRTYNIDLGSKIQF  846
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